

- 57 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: (OTHER THAN US): The Council of The Queensland Institute of Medical Research  
(US ONLY): HAYWARD Nicholas, SILINS Ginters, GRIMMOND Sean, GARTSIDE Michael and HANCOCK, John

(ii) TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 45

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE  
(B) STREET: 1 LITTLE COLLINS STREET  
(C) CITY: MELBOURNE  
(D) STATE: VICTORIA  
(E) COUNTRY: AUSTRALIA  
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT INTERNATIONAL  
(B) FILING DATE: 22-MAY-1998  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO6973  
(B) FILING DATE: 23-MAY-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 23-MAY-1997  
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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO6972  
(B) FILING DATE: 23-MAY-1997

## (C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PP1459
- (B) FILING DATE: 22-JAN-1998
- (C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PP1460
- (B) FILING DATE: 22-JAN-1998
- (C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PP1458
- (B) FILING DATE: 22-JAN-1998
- (C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: HUGHES, DR E JOHN L
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## (ix) TELECOMMUNICATION INFORMATION:

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- (C) TELEX: AA 31787

CONFIDENTIAL DOCUMENT

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Cys Xaa Xaa Cys Xaa Gly Xaa Gly  
5

## (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 30..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCAGTAAACCA CAGAGACTGG GGATCGATC ATG GGG CTT TGT AAG TGC CCC AAG Met Gly Leu Cys Lys Cys Pro Lys	53
1 5	
AGA AAG GTG ACC AAC CTG TTC TGC GAA CAT CGG GTC AAC GTC TGC Arg Lys Val Thr Asn Leu Phe Cys Phe Glu His Arg Val Asn Val Cys	101
10 15 20	
GAG CAC TGC CTG GTA GCC AAT CAC GCC AAG TGC ATC GTC CAG TCC TAC Glu His Cys Leu Val Ala Asn His Ala Lys Cys Ile Val Gln Ser Tyr	149
25 30 35 40	
CTG CAA TGG CTC CAA GAT AGC GAC TAC AAC CCC AAT TGC CGC CTG TGC Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn Pro Asn Cys Arg Leu Cys	197
45 50 55	
AAC ATA CCC CTG GCC AGC CGA GAG ACG ACC CGC CTT GTC TGC TAT GAT Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg Leu Val Cys Tyr Asp	245
60 65 70	
CTC TTT CAC TGG GCC CTC AAT GAA CGT GCT GCC CAG CTA CCC CGA Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro Arg	293
75 80 85	
AAC ACG GCA CCT GCC GGC TAT CAG TGC CCC AGC TGC AAT GGC CCC ATC Asn Thr Ala Pro Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly Pro Ile	341
90 95 100	
TTC CCC CCA ACC AAC CTG GCT GGC CCC GTG GCC TCC GCA CTG AGA GAG Phe Pro Pro Thr Asn Leu Ala Gly Pro Val Ala Ser Ala Leu Arg Glu	389
105 110 115 120	

- 60 -

AAG CTG GCC ACA GTC AAC TGG GCC CGG GCA GGA CTG GGC CTC CCT CTG Lys Leu Ala Thr Val Asn Trp Ala Arg Ala Gly Leu Gly Leu Pro Leu 125 130 135	437
ATC GAT GAG GTG GTG AGC CCA GAG CCC GAG CCC CTC AAC ACG TCT GAC Ile Asp Glu Val Val Ser Pro Glu Pro Glu Pro Leu Asn Thr Ser Asp 140 145 150	485
TTC TCT GAC TGG TCT AGT TTT AAT GCC AGC AGT ACC CCT GGA CCA GAG Phe Ser Asp Trp Ser Ser Phe Asn Ala Ser Ser Thr Pro Gly Pro Glu 155 160 165	533
GAG GTA GAC AGC GCC TCT GCT GCC CCA GCC TTC TAC AGC CGA GCC CCC Glu Val Asp Ser Ala Ser Ala Ala Pro Ala Phe Tyr Ser Arg Ala Pro 170 175 180	581
CGG CCC CCA GCT TCC CCA GGC CGG CCC GAG CAG CAC ACA GTG ATC CAC Arg Pro Pro Ala Ser Pro Gly Arg Pro Glu Gln His Thr Val Ile His 185 190 195 200	629
ATG GGC AAT CCT GAG CCC TTG ACT CAC GCC CCT AGG AAG GTG TAT GAT Met Gly Asn Pro Glu Pro Leu Thr His Ala Pro Arg Lys Val Tyr Asp 205 210 215	677
ACG CGG GAT GAT GAC CGG ACA CCA GGC CTC CAT GGA GAC TGT GAC GAT Thr Arg Asp Asp Asp Arg Thr Pro Gly Leu His Gly Asp Cys Asp Asp 220 225 230	725
GAC AAG TAC CGA CGT CGG CCG GCC TTG GGT TGG CTG GCC CGG CTG CTA Asp Lys Tyr Arg Arg Arg Pro Ala Leu Gly Trp Leu Ala Arg Leu Leu 235 240 245	773
AGG AGC CGG GCT GGG TCT CGG AAG CGG CCG CTG ACC CTG CTC CAG CGG Arg Ser Arg Ala Gly Ser Arg Lys Arg Pro Leu Thr Leu Leu Gln Arg 250 255 260	821
GCG GGG CTG CTG CTA CTC TTG GGA CTG CTG GGC TTC CTG GCC CTC CTT Ala Gly Leu Leu Leu Leu Gly Leu Leu Phe Leu Ala Leu Leu 265 270 275 280	869
GCC CTC ATG TCT CGC CTA GGC CGG GCC GCA GCT GAC AGC GAT CCC AAC Ala Leu Met Ser Arg Leu Gly Arg Ala Ala Ala Asp Ser Asp Pro Asn 285 290 295	917
CTG GAC CCA CTC ATG AAC CCT CAC ATC CGC GTG GGC CCC TCC TGA Leu Asp Pro Leu Met Asn Pro His Ile Arg Val Gly Pro Ser *	962
300 305 310	
GCCCCCTTGC TTGTGGCTAG GCCAGCCTAG GATGTGGTT CTGTGGAGGA GAGGCAGGGT	1022
AATGGGGAGG CTGAGGGCAC CTCTTCACTG CCCCTCTCCC TCAAGCCTAA GACACTAAGA	1082
CCCCAGACCC AAAGCCAAGT CCACCAGAGT GGCTCGCAGG CCAGGCCTGG AGTCCCCGTG	1142
GGTCAAGCAT TTGTCTTGAC TTGCTTCTC CCGGGCTCTCC AGCCTCCGAC CCCTCGCCCC	1202
ATGAAGGAGC TGGCAGGTGG AAATAAACAA CAACTTTATT	1242

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

- 61 -

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Leu Cys Lys Cys Pro Lys Arg Lys Val Thr Asn Leu Phe Cys  
 1 5 10 15

Phe Glu His Arg Val Asn Val Cys Glu His Cys Leu Val Ala Asn His  
 20 25 30

Ala Lys Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp  
 35 40 45

Tyr Asn Pro Asn Cys Arg Leu Cys Asn Ile Pro Leu Ala Ser Arg Glu  
 50 55 60

Thr Thr Arg Leu Val Cys Tyr Asp Leu Phe His Trp Ala Cys Leu Asn  
 65 70 75 80

Glu Arg Ala Ala Gln Leu Pro Arg Asn Thr Ala Pro Ala Gly Tyr Gln  
 85 90 95

Cys Pro Ser Cys Asn Gly Pro Ile Phe Pro Pro Thr Asn Leu Ala Gly  
 100 105 110

Pro Val Ala Ser Ala Leu Arg Glu Lys Leu Ala Thr Val Asn Trp Ala  
 115 120 125

Arg Ala Gly Leu Gly Leu Pro Leu Ile Asp Glu Val Val Ser Pro Glu  
 130 135 140

Pro Glu Pro Leu Asn Thr Ser Asp Phe Ser Asp Trp Ser Ser Phe Asn  
 145 150 155 160

Ala Ser Ser Thr Pro Gly Pro Glu Glu Val Asp Ser Ala Ser Ala Ala  
 165 170 175

Pro Ala Phe Tyr Ser Arg Ala Pro Arg Pro Pro Ala Ser Pro Gly Arg  
 180 185 190

Pro Glu Gln His Thr Val Ile His Met Gly Asn Pro Glu Pro Leu Thr  
 195 200 205

His Ala Pro Arg Lys Val Tyr Asp Thr Arg Asp Asp Asp Arg Thr Pro  
 210 215 220

Gly Leu His Gly Asp Cys Asp Asp Asp Lys Tyr Arg Arg Arg Pro Ala  
 225 230 235 240

Leu Gly Trp Leu Ala Arg Leu Leu Arg Ser Arg Ala Gly Ser Arg Lys  
 245 250 255

Arg Pro Leu Thr Leu Leu Gln Arg Ala Gly Leu Leu Leu Leu Gly  
 260 265 270

Leu Leu Gly Phe Leu Ala Leu Leu Ala Leu Met Ser Arg Leu Gly Arg  
 275 280 285

Ala Ala Ala Asp Ser Asp Pro Asn Leu Asp Pro Leu Met Asn Pro His  
 290 295 300

Ile Arg Val Gly Pro Ser  
 305 310

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..2188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CG ATT TCA TTC CTC GCT CCC CAC AGG TCC CTC TCC CCA AAA TAT TCC	47
Ile Ser Phe Leu Ala Pro His Arg Ser Leu Ser Pro Lys Tyr Ser	
1 5 10 15	
CAT CTT GTC CTA GCC CAT CCC CCA GAC TAT CTC AAG GAC CAG CTG TCC	95
His Leu Val Leu Ala His Pro Pro Asp Tyr Leu Lys Asp Gln Leu Ser	
20 25 30	
CCA CGC CCC CGA CCT CCA CTA GGC CTG TGC CAC CCG CTG CCT GCA GGA	143
Pro Arg Pro Arg Pro Pro Leu Gly Leu Cys His Pro Leu Pro Ala Gly	
35 40 45	
AGA CGC CCG GTC CCG GGC CGG GTT AGC CCC ATG GGA ACG CAG CGC CTG	191
Arg Arg Pro Val Pro Gly Arg Val Ser Pro Met Gly Thr Gln Arg Leu	
50 55 60	
TGT GCC CGC GGG ACT CAA GGC TGG CCT GGC TCA AGT GAA CAG CAC GTC	239
Cys Gly Arg Gly Thr Gln Gly Trp Pro Gly Ser Ser Glu Gln His Val	
65 70 75	
CAG GAG GCG ACC TCG TCC GCG GGT TTG CAT TCT GGG GTG GAC GAG CTG	287
Gln Glu Ala Thr Ser Ser Ala Gly Leu His Ser Gly Val Asp Glu Leu	
80 85 90 95	
GGG GTT CGG TCC GAG CCC GGT GGG AGG CTC CCG GAG CGC AGC CTG GGC	335
Gly Val Arg Ser Glu Pro Gly Arg Leu Pro Glu Arg Ser Leu Gly	
100 105 110	
CCA GCC CAC CCC GCG CCG GCC ATG GCA GGC ACC CTG GAC CTG GAC	383
Pro Ala His Pro Ala Pro Ala Met Ala Gly Thr Leu Asp Leu Asp	
115 120 125	
AAG GGC TGC ACG GTG GAG GAG CTG CTC CGC GGG TGC ATC GAA GCC TTC	431
Lys Gly Cys Thr Val Glu Glu Leu Leu Arg Gly Cys Ile Glu Ala Phe	
130 135 140	
GAT GAC TCC GGG AAG GTG CGG GAC CCG CAG CTG GTG CGC ATG TTC CTC	479
Asp Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val Arg Met Phe Leu	
145 150 155	
ATG ATG CAC CCC TGG TAC ATC CCC TCC TCT CAG CTG GCG GCC AAG CTG	527
Met Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu Ala Ala Lys Leu	
160 165 170 175	
CTC CAC ATC TAC CAA CAA TCC CCG AAG GAC AAC TCC AAT TCC CTG CAG	575
Leu His Ile Tyr Gln Gln Ser Arg Lys Asp Asn Ser Asn Ser Leu Gln	
180 185 190	
GTG AAA ACG TGC CAC CTG GTC AGG TAC TGG ATC TCC GCC TTC CCA GCG	623
Val Lys Thr Cys His Leu Val Arg Tyr Trp Ile Ser Ala Phe Pro Ala	
195 200 205	

- 63 -

GAG TTT GAC TTG AAC CCG GAG TTG GCT GAG CAG ATC AAG GAG CTG AAG Glu Phe Asp Leu Asn Pro Glu Leu Ala Glu Gln Ile Lys Glu Leu Lys 210 215 220	671
GCT CTG CTA GAC CAA GAA GGG AAC CGA CGG CAC AGC AGC CTA ATC GAC Ala Leu Leu Asp Gln Glu Gly Asn Arg Arg His Ser Ser Leu Ile Asp 225 230 235	719
ATA GAC AGC GTC CCT ACC TAC AAG TGG AAG CGG CAG GTG ACT CAG CGG Ile Asp Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln Val Thr Gln Arg 240 245 250 255	767
AAC CCT GTG GGA CAG AAA AAG CGC AAG ATG TCC CTG TTG TTT GAC CAC Asn Pro Val Gly Gln Lys Lys Arg Lys Met Ser Leu Leu Phe Asp His 260 265 270	815
CTG GAG CCC ATG GAG CTG GCG GAG CAT CTC ACC TAC TTG GAG TAT CGC Leu Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr Leu Glu Tyr Arg 275 280 285	863
TCC TTC TGC AAG ATC CTG TTT CAG GAC TAT CAC AGT TTC GTG ACT CAT Ser Phe Cys Lys Ile Leu Phe Gln Asp Tyr His Ser Phe Val Thr His 290 295 300	911
GGC TGC ACT GTG GAC AAC CCC GTC CTG GAG CGG TTC ATC TCC CTC TTC Gly Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe Ile Ser Leu Phe 305 310 315	959
AAC AGC GTC TCA CAG TGG GTG CAG CTC ATG ATC CTC AGC AAA CCC ACA Asn Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu Ser Lys Pro Thr 320 325 330 335	1007
GCC CCG CAG CGG GCC CTG GTC ATC ACA CAC TTT GTC CAC GTG GCG GAG Ala Pro Gln Arg Ala Leu Val Ile Thr His Phe Val His Val Ala Glu 340 345 350	1055
AAG CTG CTA CAG CTG CAG AAC TTC AAC ACG CTG ATG GCA GTG GTC GGG Lys Leu Leu Gln Leu Gln Asn Phe Asn Thr Leu Met Ala Val Val Gly 355 360 365	1103
GGC CTG AGC CAC AGC TCC ATC TCC CGC CTC AAG GAG ACC CAC AGC CAC Gly Leu Ser His Ser Ile Ser Arg Leu Lys Glu Thr His Ser His 370 375 380	1151
GTT AGC CCT GAG ACC ATC AAG CTC TGG GAG GGT CTC ACG GAA CTA GTG Val Ser Pro Glu Thr Ile Lys Leu Trp Glu Gly Leu Thr Glu Leu Val 385 390 395	1199
ACG GCG ACA GGC AAC TAT GGC AAC TAC CGG CGT CGG CTG GCA GCC TGT Thr Ala Thr Gly Asn Tyr Gly Asn Tyr Arg Arg Arg Leu Ala Ala Cys 400 405 410 415	1247
GTC GGC TTC CGC TTC CCG ATC CTG GGT GTG CAC CTC AAG GAC CTG GTG Val Gly Phe Arg Phe Pro Ile Leu Gly Val His Leu Lys Asp Leu Val 420 425 430	1295
GCC CTG CAG CTG GCA CTG CCT GAC TGG CTG GAC CCA GCC CGG ACC CGG Ala Leu Gln Leu Ala Leu Pro Asp Trp Leu Asp Pro Ala Arg Thr Arg 435 440 445	1343
CTC AAC GGG GCC AAG ATG AAG CAG CTC TTT AGC ATC CTG GAG GAG CTG Leu Asn Gly Ala Lys Met Lys Gln Leu Phe Ser Ile Leu Glu Glu Leu 450 455 460	1391
GCC ATG GTG ACC AGC CTG CGG CCA CCA GTA CAG GCC AAC CCC GAC CTG Ala Met Val Thr Ser Leu Arg Pro Pro Val Gln Ala Asn Pro Asp Leu 465 470 475	1439

- 64 -

CTG AGC CTG CTC ACG GTG TCT CTG GAT CAG TAT CAG ACG GAG GAT GAG Leu Ser Leu Leu Thr Val Ser Leu Asp Gln Tyr Gln Thr Glu Asp Glu 480 485 490 495	1487
CTG TAC CAG CTG TCC CTG CAG CGG GAG CCG CGC TCC AAG TCC TCG CCA Leu Tyr Gln Leu Ser Leu Gln Arg Glu Pro Arg Ser Lys Ser Ser Pro 500 505 510	1535
ACC AGC CCC ACG AGT TGC ACC CCA CCA CCC CGG CCC CCG GTC CTG GAG Thr Ser Pro Thr Ser Cys Thr Pro Pro Arg Pro Pro Val Leu Glu 515 520 525	1583
GAG TGG ACC TCG GCT GCC AAA CCC AAG CTG GAT CAG GCC CTC GTG GTG Glu Trp Thr Ser Ala Ala Lys Pro Lys Leu Asp Gln Ala Leu Val Val 530 535 540	1631
GAG CAC ATC GAG AAG ATG GTG GAG TCT GTG TTC CGG AAC TTT GAC GTC Glu His Ile Glu Lys Met Val Glu Ser Val Phe Arg Asn Phe Asp Val 545 550 555	1679
GAT GCG GAT GGC CAC ATC TCA CAG GAA GAA TTC CAG ATC ATC CGT GGG Asp Gly Asp Gly His Ile Ser Gln Glu Glu Phe Gln Ile Ile Arg Gly 560 565 570 575	1727
AAC TTC CCT TAC CTC AGC GCC TTT GGG GAC CTC GAC CAG AAC CAG GAT Asn Phe Pro Tyr Leu Ser Ala Phe Gly Asp Leu Asp Gln Asn Gln Asp 580 585 590	1775
GGC TGC ATC AGC AGG GAG GAG ATG GTT TCC TAT TTC CTG CGC TCC AGC Gly Cys Ile Ser Arg Glu Glu Met Val Ser Tyr Phe Leu Arg Ser Ser 595 600 605	1823
TCT GTG TTG GGG GGG CGC ATG GGC TTC GTA CAC AAC TTC CAG GAG AGC Ser Val Leu Gly Gly Arg Met Gly Phe Val His Asn Phe Gln Glu Ser 610 615 620	1871
AAC TCC TTG CGC CCC GTC GCC TGC CGC CAC TGC AAA GCC CTG ATC CTG Asn Ser Leu Arg Pro Val Ala Cys Arg His Cys Lys Ala Leu Ile Leu 625 630 635	1919
GGC ATC TAC AAG CAG GGC CTC AAA TGC CGA GCC TGT GGA GTG AAC TGC Gly Ile Tyr Lys Gln Gly Leu Lys Cys Arg Ala Cys Gly Val Asn Cys 640 645 650 655	1967
CAC AAG CAG TGC AAG GAT CGC CTG TCA GTT GAG TGT CGG CGC AGG GCC His Lys Gln Cys Lys Asp Arg Leu Ser Val Glu Cys Arg Arg Arg Ala 660 665 670	2015
CAG AGT GTG AGC CTG GAG GGG TCT CCA CCC TCA CCC TCA CCC ATG CAC Gln Ser Val Ser Leu Glu Gly Ser Ala Pro Ser Pro Ser Pro Met His 675 680 685	2063
AGC CAC CAT CAC CGC GCC TTC AGC TTC TCT CTG CCC CGC CCT GGC AGG Ser His His Arg Ala Phe Ser Phe Ser Leu Pro Arg Pro Gly Arg 690 695 700	2111
CGA GGC TCC AGG CCT CCA GAG ATC CGT GAG GAG GAG GTC CAG ACG GTG Arg Gly Ser Arg Pro Pro Glu Ile Arg Glu Glu Glu Val Gln Thr Val 705 710 715	2159
GAG GAT GGG GTG TTT GAC ATC CAC TTG TA ATAGATGCTG TGGTTGGATC Glu Asp Gly Val Phe Asp Ile His Leu 720 725	2208
AAGGACTCAT TCCTGCCCTTG GAGAAAATAC TTCAACCAGA GCAGGGAGCC TGGGGGTGTC	2268
GGGGCAGGAG GCTGGGGATG GGGGTGGAT ATGAGGGTGG CATGCAGCTG AGGGCAGGGC	2328

- 65 -

CAGGGCTGGT GTCCCTAAGG TTGTACAGAC TCTTGTGAAT ATTTGTATTT TCCAGATGGA	2388
ATAAAAAAGGC CCGTGTAATT AACCTTC	2415

## (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ile Ser Phe Leu Ala Pro His Arg Ser Leu Ser Pro Lys Tyr Ser His	
1 5 10 15	
Leu Val Leu Ala His Pro Pro Asp Tyr Leu Lys Asp Gln Leu Ser Pro	
20 25 30	
Arg Pro Arg Pro Pro Leu Gly Leu Cys His Pro Leu Pro Ala Gly Arg	
35 40 45	
Arg Pro Val Pro Gly Arg Val Ser Pro Met Gly Thr Gln Arg Leu Cys	
50 55 60	
Gly Arg Gly Thr Gln Gly Trp Pro Gly Ser Ser Glu Gln His Val Gln	
65 70 75 80	
Glu Ala Thr Ser Ser Ala Gly Leu His Ser Gly Val Asp Glu Leu Gly	
85 90 95	
Val Arg Ser Glu Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly Pro	
100 105 110	
Ala His Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp Lys	
115 120 125	
Gly Cys Thr Val Glu Gly Leu Leu Arg Gly Cys Ile Glu Ala Phe Asp	
130 135 140	
Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val Arg Met Phe Leu Met	
145 150 155 160	
Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu Ala Ala Lys Leu Leu	
165 170 175	
His Ile Tyr Gln Gln Ser Arg Lys Asp Asn Ser Asn Ser Leu Gln Val	
180 185 190	
Lys Thr Cys His Leu Val Arg Tyr Trp Ile Ser Ala Phe Pro Ala Glu	
195 200 205	
Phe Asp Leu Asn Pro Glu Leu Ala Glu Gln Ile Lys Glu Leu Lys Ala	
210 215 220	
Leu Leu Asp Gln Glu Gly Asn Arg Arg His Ser Ser Leu Ile Asp Ile	
225 230 235 240	
Asp Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln Val Thr Gln Arg Asn	
245 250 255	
Pro Val Gly Gln Lys Lys Arg Lys Met Ser Leu Leu Phe Asp His Leu	
260 265 270	

- 66 -

Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr Leu Glu Tyr Arg Ser  
275 280 285

Phe Cys Lys Ile Leu Phe Gln Asp Tyr His Ser Phe Val Thr His Gly  
290 295 300

Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe Ile Ser Leu Phe Asn  
305 310 315 320

Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu Ser Lys Pro Thr Ala  
325 330 335

Pro Gln Arg Ala Leu Val Ile Thr His Phe Val His Val Ala Glu Lys  
340 345 350

Leu Leu Gln Leu Gln Asn Phe Asn Thr Leu Met Ala Val Val Gly Gly  
355 360 365

Leu Ser His Ser Ser Ile Ser Arg Leu Lys Glu Thr His Ser His Val  
370 375 380

Ser Pro Glu Thr Ile Lys Leu Trp Glu Gly Leu Thr Glu Leu Val Thr  
385 390 395 400

Ala Thr Gly Asn Tyr Gly Asn Tyr Arg Arg Arg Leu Ala Ala Cys Val  
405 410 415

Gly Phe Arg Phe Pro Ile Leu Gly Val His Leu Lys Asp Leu Val Ala  
420 425 430

Leu Gln Leu Ala Leu Pro Asp Trp Leu Asp Pro Ala Arg Thr Arg Leu  
435 440 445

Asn Gly Ala Lys Met Lys Gln Leu Phe Ser Ile Leu Glu Glu Leu Ala  
450 455 460

Met Val Thr Ser Leu Arg Pro Pro Val Gln Ala Asn Pro Asp Leu Leu  
465 470 475 480

Ser Leu Leu Thr Val Ser Leu Asp Gln Tyr Gln Thr Glu Asp Glu Leu  
485 490 495

Tyr Gln Leu Ser Leu Gln Arg Glu Pro Arg Ser Lys Ser Ser Pro Thr  
500 505 510

Ser Pro Thr Ser Cys Thr Pro Pro Pro Arg Pro Pro Val Leu Glu Glu  
515 520 525

Trp Thr Ser Ala Ala Lys Pro Lys Leu Asp Gln Ala Leu Val Val Glu  
530 535 540

His Ile Glu Lys Met Val Glu Ser Val Phe Arg Asn Phe Asp Val Asp  
545 550 555 560

Gly Asp Gly His Ile Ser Gln Glu Glu Phe Gln Ile Ile Arg Gly Asn  
565 570 575

Phe Pro Tyr Leu Ser Ala Phe Gly Asp Leu Asp Gln Asn Gln Asp Gly  
580 585 590

Cys Ile Ser Arg Glu Glu Met Val Ser Tyr Phe Leu Arg Ser Ser Ser  
595 600 605

Val Leu Gly Gly Arg Met Gly Phe Val His Asn Phe Gln Glu Ser Asn  
610 615 620

Ser Leu Arg Pro Val Ala Cys Arg His Cys Lys Ala Leu Ile Leu Gly

- 67 -

625	630	635	640
Ile Tyr Lys Gln Gly Leu Lys Cys Arg Ala Cys Gly Val Asn Cys His			
645	650	655	
Lys Gln Cys Lys Asp Arg Leu Ser Val Glu Cys Arg Arg Arg Ala Gln			
660	665	670	
Ser Val Ser Leu Glu Gly Ser Ala Pro Ser Pro Ser Pro Met His Ser			
675	680	685	
His His His Arg Ala Phe Ser Phe Ser Leu Pro Arg Pro Gly Arg Arg			
690	695	700	
Gly Ser Arg Pro Pro Glu Ile Arg Glu Glu Val Gln Thr Val Glu			
705	710	715	720
Asp Gly Val Phe Asp Ile His Leu			
725			

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2309 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 254..2083

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGATTCATT CCTCGCTCCC CACAGGTCCC TCTCCCCAAA ATATTCCCAT CTTGTCCTAG	60
CCCATCCCCC AGACTATCTC AAGGACCAGC TGTCCCCACG CCCCCGACCT CCACTAGGCC	120
TGTGCCACCC GCTGCCTGCA GGAAGACGCC CGGTCCCGGG CGGGGTTAGC CCCATGGGAA	180
CGGGGTTTCGG TCCGAGCCCG GTGGGAGGCT CCCGGAGGCC AGCCTGGGCC CAGCCCACCC	240
CGCGCCGGCG GCC ATG GCA GGC ACC CTG GAC CTG GAC AAG GGC TGC ACG Met Ala Gly Thr Leu Asp Leu Asp Lys Gly Cys Thr	289
1 5 10	
GTG GAG GAG CTG CTC CGC GGG TGC ATC GAA GCC TTC GAT GAC TCC GGG Val Glu Glu Leu Leu Arg Gly Cys Ile Glu Ala Phe Asp Asp Ser Gly	337
15 20 25	
AAG GTG CGG GAC CCG CAG CTG GTG CGC ATG TTC CTC ATG ATG CAC CCC Lys Val Arg Asp Pro Gln Leu Val Arg Met Phe Leu Met Met His Pro	385
30 35 40	
TGG TAC ATC CCC TCC TCT CAG CTG GCG GCC AAG CTG CTC CAC ATC TAC Trp Tyr Ile Pro Ser Ser Gln Leu Ala Ala Lys Leu Leu His Ile Tyr	433
45 50 55 60	
CAA CAA TCC CGG AAG GAC AAC TCC AAT TCC CTG CAG GTG AAA ACG TGC Gln Gln Ser Arg Lys Asp Asn Ser Asn Ser Leu Gln Val Lys Thr Cys	481
65 70 75	
CAC CTG GTC AGG TAC TCG ATC TCC GCC TTC CCA GCG GAG TTT GAC TTG	529

His Leu Val Arg Tyr Trp Ile Ser Ala Phe Pro Ala Glu Phe Asp Leu		
80	85	90
AAC CCG GAG TTG GCT GAG CAG ATC AAG GAG CTG AAG GCT CTG CTA GAC		577
Asn Pro Glu Leu Ala Glu Gln Ile Lys Glu Leu Lys Ala Leu Leu Asp		
95	100	105
CAA GAA GGG AAC CGA CGG CAC AGC AGC CTA ATC GAC ATA GAC AGC GTC		625
Gln Glu Gly Asn Arg Arg His Ser Ser Leu Ile Asp Ile Asp Ser Val		
110	115	120
CCT ACC TAC AAG TGG AAG CGG CAG GTG ACT CAG CGG AAC CCT GTG GGA		673
Pro Thr Tyr Lys Trp Lys Arg Gln Val Thr Gln Arg Asn Pro Val Gly		
125	130	135
140		
CAG AAA AAG CGC AAG ATG TCC CTG TTG TTT GAC CAC CTG GAG CCC ATG		721
Gln Lys Lys Arg Lys Met Ser Leu Leu Phe Asp His Leu Glu Pro Met		
145	150	155
GAG CTG GCG GAG CAT CTC ACC TAC TTG GAG TAT CGC TCC TTC TGC AAG		769
Glu Leu Ala Glu His Leu Thr Tyr Leu Glu Tyr Arg Ser Phe Cys Lys		
160	165	170
ATC CTG TTT CAG GAC TAT CAC AGT TTC GTG ACT CAT GGC TGC ACT GTG		817
Ile Leu Phe Gln Asp Tyr His Ser Phe Val Thr His Gly Cys Thr Val		
175	180	185
GAC AAC CCC GTC CTG GAG CGG TTC ATC TCC CTC TTC AAC AGC GTC TCA		865
Asp Asn Pro Val Leu Glu Arg Phe Ile Ser Leu Phe Asn Ser Val Ser		
190	195	200
CAG TGG GTG CAG CTC ATG ATC CTC AGC AAA CCC ACA GCC CCG CAG CGG		913
Gln Trp Val Gln Leu Met Ile Leu Ser Lys Pro Thr Ala Pro Gln Arg		
205	210	215
220		
GCC CTG GTC ATC ACA CAC TTT GTC CAC GTG GCG GAG AAG CTG CTA CAG		961
Ala Leu Val Ile Thr His Phe Val His Val Ala Glu Lys Leu Leu Gln		
225	230	235
CTG CAG AAC TTC AAC ACG CTG ATG GCA GTG GTC GGG GGC CTG AGC CAC		1009
Leu Gln Asn Phe Asn Thr Leu Met Ala Val Val Gly Gly Leu Ser His		
240	245	250
AGC TCC ATC TCC CGC CTC AAG GAG ACC CAC AGC CAC GTT AGC CCT GAG		1057
Ser Ser Ile Ser Arg Leu Lys Glu Thr His Ser His Val Ser Pro Glu		
255	260	265
ACC ATC AAG CTC TGG GAG GGT CTC ACG GAA CTA GTG ACG GCG ACA GGC		1105
Thr Ile Lys Leu Trp Glu Gly Leu Thr Glu Leu Val Thr Ala Thr Gly		
270	275	280
AAC TAT GGC AAC TAC CGG CGT CGG CTG GCA GCC TGT GTG GGC TTC CGC		1153
Asn Tyr Gly Asn Tyr Arg Arg Leu Ala Ala Cys Val Gly Phe Arg		
285	290	295
300		
TTC CCG ATC CTG GGT GTG CAC CTC AAG GAC CTG GTG GCC CTG CAG CTG		1201
Phe Pro Ile Leu Gly Val His Leu Lys Asp Leu Val Ala Leu Gln Leu		
305	310	315
GCA CTG CCT GAC TGG CTG GAC CCA GCC CGG ACC CGG CTC AAC GGG GCC		1249
Ala Leu Pro Asp Trp Leu Asp Pro Ala Arg Thr Arg Leu Asn Gly Ala		
320	325	330
AAG ATG AAG CAG CTC TTT AGC ATC CTG GAG GAG CTG GCC ATG GTG ACC		1297
Lys Met Lys Gln Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr		
335	340	345

AGC CTG CGG CCA CCA GTA CAG GCC AAC CCC GAC CTG CTG AGC CTG CTC Ser Leu Arg Pro Pro Val Gln Ala Asn Pro Asp Leu Leu Ser Leu Leu 350 355 360	1345
ACG GTG TCT CTG GAT CAG TAT CAG ACG GAG GAT GAG CTG TAC CAG CTG Thr Val Ser Leu Asp Gln Tyr Gln Thr Glu Asp Glu Leu Tyr Gln Leu 365 370 375 380	1393
TCC CTG CAG CGG GAG CCG CGC TCC AAG TCC TCG CCA ACC AGC CCC ACG Ser Leu Gln Arg Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr 385 390 395	1441
AGT TGC ACC CCA CCA CCC CGG CCC CCG GTA CTG GAG GAG TGG ACC TCG Ser Cys Thr Pro Pro Pro Arg Pro Val Leu Glu Glu Trp Thr Ser 400 405 410	1489
GCT GCC AAA CCC AAG CTG GAT CAG GCC CTC GTG GTG GAG CAC ATC GAG Ala Ala Lys Pro Lys Leu Asp Gln Ala Leu Val Val Glu His Ile Glu 415 420 425	1537
AAG ATG GTG GAG TCT GTG TTC CGG AAC TTT GAC GTC GAT GGG GAT GGC Lys Met Val Glu Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly 430 435 440	1585
CAC ATC TCA CAG GAA GAA TTC CAG ATC ATC CGT GGG AAC TTC CCT TAC His Ile Ser Gln Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr 445 450 455 460	1633
CTC AGC GCC TTT GGG GAC CTC GAC CAG AAC CAG GAT GGC TGC ATC AGC Leu Ser Ala Phe Gly Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser 465 470 475	1681
AGG GAG GAG ATG GTT TCC TAT TTC CTG CGC TCC AGC TCT GTG TTG GGG Arg Glu Glu Met Val Ser Tyr Phe Leu Arg Ser Ser Val Leu Gly 480 485 490	1729
GGG CGC ATG GGC TTC GTA CAC AAC TTC CAG GAG AGC AAC TCC TTG CGC Gly Arg Met Gly Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg 495 500 505	1777
CCC GTC GCC TGC CGC CAC TGC AAA GCC CTG ATC CTG GGC ATC TAC AAG Pro Val Ala Cys Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys 510 515 520	1825
CAG GGC CTC AAA TGC CGA GCC TGT GGA GTG AAC TGC CAC AAG CAG TGC Gln Gly Leu Lys Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys 525 530 535 540	1873
AAG GAT CGC CTG TCA GTT GAG TGT CGG CGC AGG GCC CAG AGT GTG AGC Lys Asp Arg Leu Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser 545 550 555	1921
CTG GAG GGG TCT GCA CCC TCA CCC TCA CCC ATG CAC AGC CAC CAT CAC Leu Glu Gly Ser Ala Pro Ser Pro Ser Pro Met His Ser His His His 560 565 570	1969
CGC GCC TTC AGC TTC TCT CTG CCC CGC CCT GGC AGG CGA GGC TCC AGG Arg Ala Phe Ser Phe Ser Leu Pro Arg Pro Gly Arg Arg Gly Ser Arg 575 580 585	2017
CCT CCA GAG ATC CGT GAG GAG GAC GTC CAG ACG GTG GAG GAT GGG GTG Pro Pro Glu Ile Arg Glu Glu Val Gln Thr Val Glu Asp Gly Val 590 595 600	2065
TTT GAC ATC CAC TTG TAATAGATCC TGTGGTTGGA TCAAGGACTC ATTCCTGCCT Phe Asp Ile His Leu 605 610	2120

- 70 -

TGGAGAAAAT ACTTCAACCA GAGCAGGGAG CCTGGGGGTG TCGGGGCAGG AGGCTGGGA	2180
TGGGGGTGGG ATATGAGGGT GGCATGCAGC TGAGGGCAGG GCCAGGGCTG GTGTCCCTAA	2240
GGTTGTACAG ACTCTTGTGA ATATTTGTAT TTTCCAGATG CAATAAAAAG GCCCGTGTAA	2300
TTAACCTTC	2309

## (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Gly Thr Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu Leu	
1 5 10 15	
Leu Arg Gly Cys Ile Glu Ala Phe Asp Asp Ser Gly Lys Val Arg Asp	
20 25 30	
Pro Gln Leu Val Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro	
35 40 45	
Ser Ser Gln Leu Ala Ala Lys Leu Leu His Ile Tyr Gln Gln Ser Arg	
50 55 60	
Lys Asp Asn Ser Asn Ser Leu Gln Val Lys Thr Cys His Leu Val Arg	
65 70 75 80	
Tyr Trp Ile Ser Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu	
85 90 95	
Ala Glu Gln Ile Lys Glu Leu Lys Ala Leu Leu Asp Gln Glu Gly Asn	
100 105 110	
Arg Arg His Ser Ser Leu Ile Asp Ile Asp Ser Val Pro Thr Tyr Lys	
115 120 125	
Trp Lys Arg Gln Val Thr Gln Arg Asn Pro Val Gly Gln Lys Lys Arg	
130 135 140	
Lys Met Ser Leu Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu	
145 150 155 160	
His Leu Thr Tyr Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln	
165 170 175	
Asp Tyr His Ser Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val	
180 185 190	
Leu Glu Arg Phe Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln	
195 200 205	
Leu Met Ile Leu Ser Lys Pro Thr Ala Pro Gln Arg Ala Leu Val Ile	
210 215 220	
Thr His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe	
225 230 235 240	
Asn Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser	
245 250 255	

- 71 -

Arg Leu Lys Glu Thr His Ser His Val Ser Pro Glu Thr Ile Lys Leu  
260 265 270

Trp Glu Gly Leu Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Gly Asn  
275 280 285

Tyr Arg Arg Arg Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu  
290 295 300

Gly Val His Leu Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp  
305 310 315 320

Trp Leu Asp Pro Ala Arg Thr Arg Leu Asn Gly Ala Lys Met Lys Gln  
325 330 335

Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro  
340 345 350

Pro Val Gln Ala Asn Pro Asp Leu Leu Ser Leu Leu Thr Val Ser Leu  
355 360 365

Asp Gln Tyr Gln Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg  
370 375 380

Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro  
385 390 395 400

Pro Pro Arg Pro Pro Val Leu Glu Glu Trp Thr Ser Ala Ala Lys Pro  
405 410 415

Lys Leu Asp Gln Ala Leu Val Val Glu His Ile Glu Lys Met Val Glu  
420 425 430

Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln  
435 440 445

Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe  
450 455 460

Gly Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met  
465 470 475 480

Val Ser Tyr Phe Leu Arg Ser Ser Val Leu Gly Gly Arg Met Gly  
485 490 495

Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys  
500 505 510

Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys  
515 520 525

Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu  
530 535 540

Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser  
545 550 555 560

Ala Pro Ser Pro Ser Pro Met His Ser His His Arg Ala Phe Ser  
565 570 575

Phe Ser Leu Pro Arg Pro Gly Arg Arg Gly Ser Arg Pro Pro Glu Ile  
580 585 590

Arg Glu Glu Glu Val Gln Thr Val Glu Asp Gly Val Phe Asp Ile His  
595 600 605

Leu

## (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 11..733

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCCCGCCGCC	ATG CCG CCC TTA CTG CCC CTG CGC CTG TGC CGG CTG TGG	49
	Met Pro Pro Leu Leu Pro Leu Arg Leu Cys Arg Leu Trp	
1	5	10
CCC CGC AAC CCT CCC TCC CGG CTC CTC GGA GCG GCC GCC	GGG CAG CGG	97
Pro Arg Asn Pro Pro Ser Arg Leu Leu Gly Ala Ala Ala	Gly Gln Arg	
15	20	25
TCC AGA CCC AGT ACT TAT TAT GAA CTG TTG GGG GTG CAT CCT GGT GCC	145	
Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala		
30	35	40
AGC ACT GAG GAA GTT AAA CGA GCT TTC TCC AAG TCC AAA GAG CTG	193	
Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu		
50	55	60
CAC CCA GAC CGG GAC CCT GGG AAC CCA AGC CTG CAC AGC CGC TTT GTG	241	
His Pro Asp Arg Asp Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val		
65	70	75
GAG CTG AGC GAG GCA TAC CGT GTG CTC AGC CGT GAG CAG AGC CGC CGC	289	
Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln Ser Arg Arg		
80	85	90
AGC TAT GAT GAC CAG CTC CGC TCA GGT AGT CCC CCA AAG TCT CCA CGA	337	
Ser Tyr Asp Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys Ser Pro Arg		
95	100	105
ACC ACA GTC CAT GAC AAG TCT GCC CAC CAA ACA CAC AGC TCC TGG ACA	385	
Thr Thr Val His Asp Lys Ser Ala His Gln Thr His Ser Ser Trp Thr		
110	115	120
125		
CCC CCC AAC GCA CAG TAC TGG TCC CAG TTT CAC AGC GTG AGG CCA CAG	433	
Pro Pro Asn Ala Gln Tyr Trp Ser Gln Phe His Ser Val Arg Pro Gln		
130	135	140
GGG CCC CAG TTG AGG CAG CAG CAA CAC AAA CAA AAC AAA CAA GTG CTG	481	
Gly Pro Gln Leu Arg Gln Gln His Lys Gln Asn Lys Gln Val Leu		
145	150	155
GGG TAC TGC CTC CTC ATG CTG GCG GGC ATG GGC CTG CAC TAC ATT	529	
Gly Tyr Cys Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile		
160	165	170
GCC TTC AGG AAG GTG AAG CAG ATG CAC CTT AAC TTC ATG GAT GAA AAG	577	
Ala Phe Arg Lys Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys		
175	180	185

- 73 -

GAT CGG ATC ATC ACA GCC TTC TAC AAC GAA GCC CGG GCA CGG GCC AGG	625
Asp Arg Ile Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg	
190 195 200 205	
GCC AAC AGA GGC ATC CTT CAG CAG GAG CGA CAA CGG CTA GGG CAG CGG	673
Ala Asn Arg Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg	
210 215 220	
CAG CCG CCA CCA TCC GAG CCA ACC CAA GGC CCC GAG ATC GTG CCC CGG	721
Gln Pro Pro Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val Pro Arg	
225 230 235	
GGC GCC GGC CCC TGA GGGGCTC ACCTGGATGG GGCCTGCAGT GCGTTCCCGC	773
Gly Ala Gly Pro *	
240	
TTTGCTTCCT TCCCTGGACG GCCCCCTCCC CGAAACGCGC GCAATAAACT GATTGGCAG	832

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Pro Leu Leu Pro Leu Arg Leu Cys Arg Leu Trp Pro Arg Asn	
1 5 10 15	
Pro Pro Ser Arg Leu Leu Gly Ala Ala Gly Gln Arg Ser Arg Pro	
20 25 30	
Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu	
35 40 45	
Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp	
50 55 60	
Arg Asp Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val Glu Leu Ser	
65 70 75 80	
Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln Ser Arg Arg Ser Tyr Asp	
85 90 95	
Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys Ser Pro Arg Thr Thr Val	
100 105 110	
His Asp Lys Ser Ala His Gln Thr His Ser Ser Trp Thr Pro Pro Asn	
115 120 125	
Ala Gln Tyr Trp Ser Gln Phe His Ser Val Arg Pro Gln Gly Pro Gln	
130 135 140	
Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln Val Leu Gly Tyr Cys	
145 150 155 160	
Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile Ala Phe Arg	
165 170 175	
Lys Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys Asp Arg Ile	
180 185 190	
Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Asn Arg	

- 74 -

195

200

205

Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg Gln Pro Pro  
 210 215 220

Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val Pro Arg Gly Ala Gly  
 225 230 235 240

Pro

SEQ ID Nos: 10-18 25-36

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 300 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 170..300

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTCACT CCTCGCTCCC CACAGGTCCC TCTCCCCAAA ATATTCCCAT CTTGTCCTAG 60  
 CCCATCCCCC AGACTATCTC AAGGACCAGC TGTCCCCACG CCCCCCGACCT CCACTAGGCC 120  
 TGTGCCACCC GCTGCCCTGCA GGAAGACGCC CGGTCCCCGGG CCGGGTTAG CCC CAT 175  
 Pro His  
 1

GGG AAC CGG GTT CGG TCC GAG CCC GGT GGG AGG CTC CCG GAG CGC AGC 223  
 Gly Asn Gly Val Arg Ser Glu Pro Gly Gly Arg Leu Pro Glu Arg Ser  
 5 10 15

CTG GGC CCA GCC CAC CCC GCG CCG GCG GCC ATG GCA GGC ACC CTG GAC 271  
 Leu Gly Pro Ala His Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp  
 20 25 30

CTG GAC AAG GGC TGC ACG GTG GAG GAG CT 300  
 Leu Asp Lys Gly Cys Thr Val Glu Glu Leu  
 35 40

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

- 75 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro His Gly Asn Gly Val Arg Ser Glu Pro Gly Gly Arg Leu Pro Glu  
1 5 10 15  
Arg Ser Leu Gly Pro Ala His Pro Ala Pro Ala Ala Met Ala Gly Thr  
20 25 30  
Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGATCCCCC TGGTC 15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Val Asp Glu Glu Asp Glu Val Glu Asp Ile Glu Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Val Asp Gly Asp Gly His Ile Ser Gln Glu Glu Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids

- 76 -

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp His Asp Arg Asp Gly Phe Ile Ser Gln Glu Glu Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asp Val Asp Met Asp Gly Gln Ile Ser Lys Asp Glu Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe Asn  
1 5 10 15

Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser Arg  
20 25 30

- 77 -

Leu Lys Glu Thr His  
35

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys Phe Val His Val Ala Lys His Leu Arg Lys Ile Asn Asn Phe Asn  
1 5 10 15  
Thr Leu Met Ser Val Val Gly Gly Ile Thr His Ser Ser Val Ala Arg  
20 25 30  
Leu Ala Lys Thr Tyr  
35

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys Arg His  
1 5 10 15  
Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys Cys Arg  
20 25 30  
Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu Ser Val  
35 40 45  
Glu Cys  
50

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His Asn Phe His Glu Thr Thr Phe Leu Thr Pro Thr Cys Asn His

- 78 -

1	5	10	15												
Cys	Asn	Lys	Leu	Leu	Trp	Gly	Ile	Leu	Arg	Gln	Gly	Phe	Lys	Cys	Lys
		20						25					30		
Asp	Cys	Gly	Leu	Ala	Val	His	Ser	Cys	Cys	Lys	Ser	Asn	Ala	Val	Ala
			35				40				45				
Glu	Cys														
		50													

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGATCCCCC TGGTC 15

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCTGGCA CGAGCCGACG G 21

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 78 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGGAGCAGA AGCTGATCTC CGAGGAGGAC CTGCCGGGG CAGCTGGATC CGCAGCCCAC 60  
CCCGCGCCGG CGGCCATG 78

## (2) INFORMATION FOR SEQ ID NO:22:

- 79 -

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Pro	Gly	Ala	Ala	Gly
1				5					10					15	
Ser Ala Ala His Pro Ala Pro Ala Ala Met															
20 25															

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCCGCAG CCCACCCCGC GCCGGCGGCC ATG

33

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gly Ser Ala Ala His Pro Ala Pro Ala Ala Met  
5 10

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- 80 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGACAAAGTG TGTGATGAAC C

21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCATCCTCC GTCTGATACT G

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTAGATGTGG ATCAGCTTGG

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGTGGAGAA TGGTCAAGG

19

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTCATAGTCT GTCTCCTACT

20

## (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ACATAGACAG CGTGCCTACC

20

## (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TACAAACCTTA GGGACACCAAG

20

## (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGCTGAGCCT GCTCACGGTG

20

## (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAGTGAAACA CCACGTCC

18

## (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- 82 -

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GACTATCTCA AGGACCAGCT G

21

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTTCCGGTCC GAGCCCCG

18

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGAGCGATAAC TCCAAGTAGG T

21

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AGCGGGGCCAG GCCCCTTC

18

(2) INFORMATION FOR SEQ ID NO:38: